

 [ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Proteomics tools](#) [Swiss-Prot](#)

Search   for

=====

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the BLAST 2 software.

In case of problems, please read the online BLAST help.  
If your question is not covered, please contact <helpdesk@expasy.org>

NCBI BLAST program reference [PMID:9254694]:  
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 80 AA  
Date run: 2006-04-25 16:35:57 UTC+0100 on blast01.vital-it.ch  
Program: NCBI BLASTP 2.2.13 [Nov-27-2005]  
Database: UniProtKB  
3,037,447 sequences; 998,712,776 total letters  
UniProt Knowledgebase Release 7.5 consists of:  
UniProtKB/Swiss-Prot Release 49.5 of 18-Apr-2006: 216380 entries  
UniProtKB/TrEMBL Release 32.5 of 18-Apr-2006: 2807081 entries

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

**List of potentially matching sequences**

Send selected sequences to



☐ Include query sequence

Db	AC	Description
----	----	-------------

- |                                     |    |        |            |  |
|-------------------------------------|----|--------|------------|--|
| <input checked="" type="checkbox"/> | sp | P11439 | TOXA_PSEAE | Exotoxin A precursor (NAD-dependent ADP-rib.     |
| <input checked="" type="checkbox"/> | tr | Q5EK40 | _VIBCH     | Hypothetical exotoxin A [toxA] [Vibrio cholerae] |

- ☒ tr Q39QN3 \_GEOMG Excinuclease ABC, C subunit [Gmet\_3228] [Geobact
- ☒ sp Q747I7 UVRC\_GEOSL UvrABC system protein C (Protein uvrC) (Exc.
- ☒ tr Q6MDL6 \_PARUW Hypothetical protein [pc0609] [Parachlamydia sp.
- ☐ tr Q40YK6 \_KINRA Phosphoesterase PHP, N-terminal:PHP, C-terminal
- ☐ tr Q6DAZ3 \_ERWCT Hypothetical protein [ECA0109] [Erwinia carotovo
- ☐ tr Q3GJU1 \_CHLVI Transposase, IS204/IS1001/IS1096/IS1165 [CvibDRA
- ☐ tr Q2E5S4 \_BACCE Hypothetical protein [Bcer98DRAFT\_0450] [Bacillu
- ☐ sp Q7TPG8 F19A1\_MOUSE Protein FAM19A1 precursor (Chemokine-like .
- ☐ sp Q7Z5A9 F19A1\_HUMAN Protein FAM19A1 precursor (Chemokine-like .
- ☐ tr Q9CPF8 \_PASMU HofB [hofB] [Pasteurella multocida]
- ☐ tr Q65L06 \_BACLD Hypothetical DNA-binding protein, putative transc
- ☐ tr Q25IT8 \_MACFA Brain cDNA, clone: QflA-18513 [Macaca fascicular
- ☐ tr Q4RFA4 \_TETNG Chromosome 8 SCAF15119, whole genome shotgun seq

### Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(?) Help) (use ScanProsite for more details about PROSITE matches)

#### Profile hits

#### Pfam hits

#### Matches on query sequence

#### Submission

TOXA\_PSEAE  
Q5EK40\_VIBCH  
Q39QN3\_GEOMG  
UVRC\_GEOSL  
Q6MDL6\_PARUW  
Q40YK6\_KINRA  
Q6DAZ3\_ERWCT  
Q3GJU1\_CHLVI  
Q2E5S4\_BACCE  
F19A1\_MOUSE  
F19A1\_HUMAN  
Q9CPF8\_PASMU  
Q65L06\_BACLD  
Q25IT8\_MACFA  
Q4RFA4\_TETNG

#### Submission

Identity 0 25 50 75 100%

### Alignments

sp P11439 Exotoxin A precursor (NAD-dependent ADP-  
TOXA\_PSEAE ribosyltransferase) (EC

## 2.4.2.-) [eta] [Pseudomonas aeruginosa]

Score = 206 bits (469), Expect = 1e-52  
 Identities = 80/80 (100%), Positives = 80/80 (100%)

Query: 1 HRLHFPEGGS LAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA  
 HRLHFPEGGS LAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA  
 Sbjct: 271 HRLHFPEGGS LAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA

Query: 61 NQVDQVIRNALASPGSGGDL 80  
 NQVDQVIRNALASPGSGGDL  
 Sbjct: 331 NQVDQVIRNALASPGSGGDL 350

tr Q5EK40 Hypothetical exotoxin A [toxA] [Vibrio cholerae] 6  
 Q5EK40\_VIBCH a

Score = 68.1 bits (149), Expect = 5e-11  
 Identities = 26/66 (39%), Positives = 42/66 (63%)

Query: 1 HRLHFPEGGS LAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA  
 +R+HF +G +++AL AH+ C +PLET R R+PR C Y Q +V+L++A  
 Sbjct: 291 QRIHFSKGNAMSALAAHRVCGVPLETLARSRKPRDLTDDLSCAYQAQNIVSLFVAT

Query: 61 NQVDQV 66  
 ++D V  
 Sbjct: 351 SHLDSV 356

tr Q39QN3 Excinuclease ABC, C subunit [Gmet\_3228] [Geobacter 614  
 Q39QN3\_GEOMG metallireducens AA  
 (strain GS-15 / ATCC 53774 / DSM 7210)] align

Score = 33.6 bits (69), Expect = 1.1  
 Identities = 14/31 (45%), Positives = 18/31 (58%)

Query: 21 HLPLETFTRHRQPRGWEQLEQCGYPVQRLVA 51  
 H PLET R R+P QL QC P + L++  
 Sbjct: 151 HYPLETCRRRRRPPCLFYQLRQCSAPCHGLIS 181

sp Q747I7 UvrABC system protein C (Protein uvrC) (Excinuclease ABC 61:  
 UVRC\_GEOSL subunit C) AA  
 [uvrC] [Geobacter sulfurreducens] al:

Score = 32.7 bits (67), Expect = 2.1

Identities = 18/51 (35%), Positives = 24/51 (47%), Gaps = 12/51 (2

Query: 21 HLPLETFTRHRQPRGWEQLEQCGYPVQRLV-----ALYLAARLS 59  
           H PLE+ R R+P QL QC P + L+ AL+LA + S  
 Sbjct: 151 HYPLESCRRRRRPFCLFYQLRQCAAPCHGLISGEDYQSLAEGAALFLAGKNS 201

tr Q6MDL6                   Hypothetical protein [pc0609] [Parachlamydia sp.  
   Q6MDL6\_PARUW            subsp.  
                           Acanthamoeba sp. (strain UWE25)]

Score = 32.3 bits (66), Expect = 2.8

Identities = 19/62 (30%), Positives = 30/62 (48%), Gaps = 12/62 (1

Query: 12 AALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVI  
           A+++AH+ + LE + R YP +L+AL ARL ++ DQ I  
 Sbjct: 91 ASVSAHEGAYYILEAGLKNR-----YPQIQLIALNTLARLQSDKADQTI

Query: 72 AS 73  
           S  
 Sbjct: 139 GS 140

tr Q40YK6                   Phosphoesterase PHP, N-terminal:PHP, C-terminal                   381  
   Q40YK6\_KINRA           [KradDRAFT\_1289]                   AA  
                           [Kineococcus radiotolerans SRS30216]                   alignr

Score = 32.3 bits (66), Expect = 2.8

Identities = 17/46 (36%), Positives = 24/46 (52%), Gaps = 2/46 (4%

Query: 32 QPRGWEQLEQCGYPVQRLVALYLAAR-LSWN-QVDQVIRNALASPG 75  
           QP G + ++CG P +R+V + A R L W Q R A +PG  
 Sbjct: 336 QPYGCARAQECGVP AERIVTTWPAERVLEWTAQRRSAHRPARPAPG 381

tr Q6DAZ3                   Hypothetical protein [ECA0109] [Erwinia carotovora  
   Q6DAZ3\_ERWCT           subsp.  
                           atroseptica (Pectobacterium atrosepticum)]

Score = 31.9 bits (65), Expect = 3.8

Identities = 22/61 (36%), Positives = 28/61 (45%), Gaps = 14/61 (2

Query: 11 LAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQV  
           +AA+ HQA HL LE H + R P +RL+ +Y R NQV

Sbjct: 259 MAAVVPHQASHLSLE----HMRKR-----LAIPTERLIDIY---RYHGNQVAAS

Query: 71 L 71

L

Sbjct: 305 L 305

tr Q3GJU1 Transposase, IS204/IS1001/IS1096/IS1165 [CvibDRAFT\_1521] 406 AA  
Q3GJU1\_CHLVI [Prosthecochloris vibrioformis DSM 265]

align

Score = 31.9 bits (65), Expect = 3.8

Identities = 11/16 (68%), Positives = 13/16 (81%)

Query: 57 RLSWNQVDQVIRNALA 72

RLSW VDQ++R ALA

Sbjct: 129 RLSWHSVDQIMRRALA 144

tr Q2E5S4 Hypothetical protein [Bcer98DRAFT\_0450] [Bacillus cereus] 172  
Q2E5S4\_BACCE subsp. AA  
cytotoxis NVH 391-98] align

Score = 31.4 bits (64), Expect = 5.1

Identities = 19/53 (35%), Positives = 28/53 (52%), Gaps = 2/53 (3%)

Query: 20 CHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNALA 72

CH LE + + + PRG G +Q V+LY RL WN ++I+ A+A

Sbjct: 22 CHEVLEELYWKLK-PRGKRDHHWVGL-IQIAVSPLYHQRRNLNWNGAAKMIKRAIA 72

sp Q7TPG8 Protein FAM19A1 precursor (Chemokine-like protein TAFA-1) 133 AA  
F19A1\_MOUSE [Fam19a1] [Mus musculus (Mouse)]

align

Score = 31.0 bits (63), Expect = 6.8

Identities = 10/20 (50%), Positives = 13/20 (65%)

Query: 1 HRLHFPEGGS LAALTAHQAC 20

H LH PEGG+ + AH+ C

Sbjct: 34 HHLHRPEGGTCEVIAAHRCC 53

sp Q7Z5A9 Protein FAM19A1 precursor (Chemokine-like protein TAFA-1) 133 AA

F19A1 HUMAN [FAM19A1] [Homo sapiens (Human)]

align

Score = 31.0 bits (63), Expect = 6.8

Identities = 10/20 (50%), Positives = 13/20 (65%)

Query: 1 HRLHFPEGGS LAALTAHQAC 20

$$H \quad LH \quad PEGG+ \quad + \quad AH+ \quad C$$

Sbjct: 34 HHLHRPEGGTCEVIAAHRCC 53

| tr | Q9CPF8 |

**HofB** [hofB] [*Pasteurella multocida*]

461 AA

Q9CPF8 PASMU

align

Score = 31.0 bits (63), Expect = 6.8

Identities = 19/55 (34%), Positives = 27/55 (49%), Gaps = 3/55 (5%)

Query: 7 EGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYP---VQRLVALYLAARL

E +L AL A O HL L T P +L+O G P +++ + L +A RL

Sbjct: 337 EESALIALRAAQTGHLVLSTLHTNDAPSALTRLOQLGVPLHEIEOSLLLVAORL

| tr | Q65L06 |

Hypothetical DNA-binding protein, putative

225

Q65L06 BACLD

transcriptional regulator

AA

[BL03804] [*Bacillus licheniformis* (strain DSM 13 / ATCC 14580)]

align

Score = 31.0 bits (63), Expect = 6.8

Identities = 12/30 (40%), Positives = 16/30 (53%)

Query: 36 WEQLEQCGYPVQRLVALYLAARLSWNQVDQ 65

W ++O P OR+ L LAA WN + O

Sbjct: 151 WAAIQOMNVFORIRFLRLAADFNWNTIHO 180

| tr | 025IT8 |

Brain cDNA, clone: Qf1A-18513 [Macaca fascicularis (Crab

133

Q25IT8 MACFA

eating

AA

macaque) (Cynomolgus monkey)]

align

Score = 31.0 bits (63), Expect = 6.8

Identities = 10/20 (50%), Positives = 13/20 (65%)

Query: 1 HRLHFPEGGS LAALTAHQAC 20

$$H \quad LH \quad PEGG+ \quad + \quad AH+ \quad C$$

Sbjct: 34 HHLHRPEGGTCEVIAAHRCC 53

```
tr      Q4RFA4          Chromosome 8 SCAF15119, whole genome shotgun :
        Q4RFA4_TETNG    sequence                                     :
                        [GSTENG00035413001] [Tetraodon nigroviridis (Green
                        puffer)]
```

Score = 30.6 bits (62), Expect = 9.2

Identities = 21/71 (29%), Positives = 33/71 (46%), Gaps = 11/71 (1

```
Query: 21  HLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQ-----
           H+P      +H+  R  E+L+  G      +      + +A+R S N VD
```

```
Sbjct: 245 HIPKTATAKHKGRREGGEELDSQGDASSQPDITISIASRTSQNTVDSKLSGGCELTV
```

```
Query: 70  ALASPGSGGDL 80
```

```
        +AS GS G+L
```

```
Sbjct: 305 FVASNGSSGEL 315
```

Database: UniProtKB

Posted date: Apr 17, 2006 4:33 PM

Number of letters in database: 996,967,394

Number of sequences in database: 3,032,459

Database: /home/local/blastnet/database/EXPASY//UniProtKB.01

Posted date: Apr 17, 2006 4:34 PM

Number of letters in database: 1,745,382

Number of sequences in database: 4988

Lambda	K	H
0.340	0.176	0.689

Gapped

Lambda	K	H
0.299	0.0710	0.270

Matrix: BLOSUM80

Gap Penalties: Existence: 10, Extension: 1

Number of Hits to DB: 129,822,965

Number of Sequences: 3037447

Number of extensions: 2444038

Number of successful extensions: 13677

Number of sequences better than 10.0: 15

Number of HSP's better than 10.0 without gapping: 9

Number of HSP's successfully gapped in prelim test: 6

Number of HSP's that attempted gapping in prelim test: 13668

Number of HSP's gapped (non-prelim): 15

length of query: 80

length of database: 998,712,776  
effective HSP length: 62  
effective length of query: 18  
effective length of database: 810,391,062  
effective search space: 14587039116  
effective search space used: 14587039116  
T: 12  
A: 25  
X1: 15 ( 7.4 bits)  
X2: 34 (14.7 bits)  
X3: 57 (24.6 bits)  
S1: 39 (21.7 bits)  
S2: 62 (30.6 bits)  
Wallclock time: 3 seconds

 [ExPASy Home page](#)   [Site Map](#)   [Search ExPASy](#)   [Contact us](#)   [Proteomics tools](#)   [Swiss-Prc](#)



[First Hit](#)   [Fwd Refs](#)   [Previous Doc](#)   [Next Doc](#)   [Go to Doc#](#)

Generate Collection

Print

L4: Entry 2 of 118

File: USPT

Apr 18, 2006

DOCUMENT-IDENTIFIER: US 7030215 B2

TITLE: Position dependent recognition of GNN nucleotide triplets by zinc fingers

## PRIOR-PUBLICATION:

DOC-ID

DATE

US 20030068675 A1

April 10, 2003

Description Paragraph (49):

Toxin molecules also have the ability to transport polypeptides across cell membranes. Often, such molecules are composed of at least two parts (called "binary toxins"): a translocation or binding domain or polypeptide and a separate toxin domain or polypeptide. Typically, the translocation domain or polypeptide binds to a cellular receptor, and then the toxin is transported into the cell. Several bacterial toxins, including Clostridium perfringens iota toxin, diphtheria toxin (DT), Pseudomonas exotoxin A (PE), pertussis toxin (PT), Bacillus anthracis toxin, and pertussis adenylate cyclase (CYA), have been used in attempts to deliver peptides to the cell cytosol as internal or amino-terminal fusions (Arora et al., J. Biol. Chem., 268:3334 3341 (1993); Perelle et al., Infect. Immun., 61:5147 5156 (1993); Stenmark et al., J. Cell Biol. 113:1025 1032 (1991); Donnelly et al., PNAS 90:3530 3534 (1993); Carbonetti et al., Abstr. Annu. Meet. Am. Soc. Microbiol. 95:295 (1995); Sebo et al., Infect. Immun. 63:3851 3857 (1995); Klimpel et al., PNAS U.S.A. 89:10277 10281 (1992); and Novak et al., J. Biol. Chem. 267:17186 17193 (1992)).

[Previous Doc](#)   [Next Doc](#)   [Go to Doc#](#)

[First Hit](#) [Fwd Refs](#)[Previous Doc](#)[Next Doc](#)[Go to Doc#](#)

Generate Collection

Print

L2: Entry 9 of 14

File: USPT

Oct 16, 2001

DOCUMENT-IDENTIFIER: US 6303120 B1

**\*\* See image for Certificate of Correction \*\***

TITLE: Synthesis of glycoconjugates of the lewis y epitope and uses thereof

## CLAIMS:

4. The method of claim 1, wherein the antibodies bind to Lewis Y expressing epithelial tumor cells.

[Previous Doc](#)[Next Doc](#)[Go to Doc#](#)

# INTERNATIONAL SEARCH REPORT

Int. Application No.

PCT/US 98/14341

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/62 A61K39/21 C07K16/10 A61K39/104 C12N15/70  
A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>EP 0 439 954 A (SERAGEN, INC.) 7 August 1991</p> <p>see page 2, line 45 - page 3, line 50 see page 4, line 1 - line 40 see page 5, line 23 - line 53 see page 11, line 35 - page 12, line 26 --- -/--</p>	<p>1-5, 7, 8, 12, 15-20, 22-24, 26-43</p>

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

27 October 1998

Date of mailing of the international search report

10/11/1998

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

Montero Lopez, B

# INTERNATIONAL SEARCH REPORT

In. tional Application No  
PCT/US 98/14341

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>VIJAY . CHAUDHARY ET AL.: "Pseudomonas exotoxin contains a specific sequence at the carboxyl terminus that is required for cytotoxicity"</p> <p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 87, no. 1, January 1990, pages 308-312, XP002079997 WASHINGTON US see abstract see page 308, right-hand column, paragraph 2</p>	1,3-5,7, 8,15-20, 22-24, 26-43
Y	<p>MAJA LUKAC ET AL.: "Toxoid of Pseudomonas aeruginosa Exotoxin A generated by deletion of an ctive site residue"</p> <p>INFECTION AND IMMUNITY., vol. 56, no. 11, November 1988, pages 3095-3098, XP002080494 WASHINGTON US see abstract</p>	2,12
A	<p>S.J. CRYZ JR ET AL.: "Human immunodeficiency virus-1 principal neutralizing domain peptide-toxin A cnjugate vaccine"</p> <p>VACCINE., vol. 13, no. 1, January 1995, pages 67-71, XP002079998 GUILDFORD GB cited in the application see abstract see page 67, left-hand column, paragraph 1 - right-hand column, paragraph 1 see page 69, left-hand column, paragraph 2 see page 70, right-hand column, paragraph 2 - page 71, left-hand column, paragraph 1</p>	
P,X	<p>DAVID J. FITZGERALD ET AL.: "Characterization of V3 loop-Pseudomonas Exotoxin chimeras"</p> <p>JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 16, 17 April 1998, pages 9951-9958, XP002079999 MD US see the whole document</p>	1-43
T	<p>WO 98 20135 A (THE GOVERNMENT OF THE UNITED STATES OF AMERICA) 14 May 1998 see page 4, line 4 - line 32 see page 22, line 40 - line 50 see page 23, line 22 - page 25, line 2 see page 27, line 18 - page 29, line 5 see page 31, line 2 - page 32, line 12</p>	

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 14341

### Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 24-26, 33-38, and 40-43  
are directed to a method of treatment of the human/animal  
body, the search has been carried out and based on the alleged  
effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such  
an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all  
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment  
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report  
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is  
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

Int l Application No

PCT/US 98/14341

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 439954 A	07-08-1991	AU 657087 B	02-03-1995
		AU 7168991 A	24-07-1991
		AU 8032194 A	27-04-1995
		CA 2071969 A	23-06-1991
		JP 5502880 T	20-05-1993
		WO 9109871 A	11-07-1991
		US 5668255 A	16-09-1997
WO 9820135 A	14-05-1998	AU 5247498 A	29-05-1998